



APR 12 2000
TECH CENTER 1600/2900
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PATENT

6/a
M.G.J.
4/13/00

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Ian S. Zagon, et al. Art Unit: 1635
Serial No.: 09/431,843 Docket: 13038
Filed: November 2, 1999 Dated: April 3, 2000
For: NOVEL NUCLEIC ACID MOLECULES
ENCODING OPIOID GROWTH FACTOR
RECEPTORS

Assistant Commissioner for Patents
Washington, DC 20231

Response to Notice to Comply under 37 C.F.R. § 1.821

Sir:

In response to the Office Communication dated February 10, 2000 and in accordance with the provisions in 37 C.F.R. §1.821, Applicants submit herewith a substitute paper and a substitute computer readable copy of the Sequence Listing, along with a Statement Under 37 C.F.R. § 1.821(f), stating that these copies are identical. A copy of the Notice to Comply is also

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8(a)

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Assistant Commissioner for Patents, Washington, DC 20231 on April 3, 2000.

Dated: April 3, 2000

Janet Giordano
Janet Giordano

enclosed. Applicants respectfully submit that the content of the paper and computer copies of the sequence listing does not introduce new matter.

Respectfully submitted,



Frank S. DiGiglio
Registration No. 31,346

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Garden City, New York 11530
(516) 742-4343

FSD/XZ:ab



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Applicants: Ian S. Zagon, et al. Art Unit: 1635
Serial No.: 09/431,843 Docket: 13038
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Assistant Commissioner for Patents
Washington, D.C. 20231

STATEMENT UNDER 37 C.F.R. § 1.821(f)

Sir:

I hereby state that the content of the substitute paper and computer readable copies of the Sequence Listing submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same.

Respectfully submitted,

Frank S. DiGiglio
Registration No. 31,346

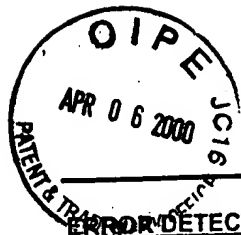
SCULLY, SCOTT, MURPHY & PRESSER
400 Garden City Plaza
Garden City, New York 11530
(516) 742-4343
FSD/XZ:ab

CERTIFICATE OF MAILING UNDER 37 C.F.R. §1.8(a)

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Janet Giordano



Raw Sequence Listing Error Summary

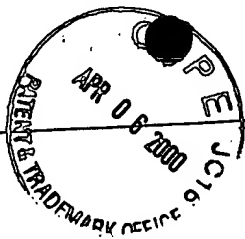
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ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☒ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
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- 10 ☐ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.



SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> Zagon S., Ian
Verderame, Michael
Allen, Sandra
McLaughlin J., Patricia

<120> NOVEL NUCLEIC ACID MOLECULES ENCODING OPIOID GROWTH
FACTOR RECEPTORS

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Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr Pro Asn Leu Ser Phe
85 90 95

Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu Asp
100 105 110

Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn His
115 120 125

Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn Trp
130 135 140

His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu Val Phe Lys Ser Ser
145 150 155 160

Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr Glu Leu Met Leu Gly
165 170 175

Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr Gly Thr Val Gly Arg
180 185 190

Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu Asn Trp Arg Ser His
195 200 205

Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser Pro Cys Glu Leu Ser
210 215 220

Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe Phe Leu Glu Glu Thr
225 230 235 240

Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln Ser Ala Leu Asp Tyr
245 250 255

Phe Met Phe Ala Val Arg Cys Arg His Gln Arg Arg Gln Leu Val His
260 265 270

Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys Phe Val Trp Gly Pro
275 280 285

Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser Leu Pro His Pro Leu
290 295 300

Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Ser Pro Gly Asp Pro Asp
305 310 315 320

His	Glu	Ala	Ser	Thr	Gln	Gly	Arg	Thr	Cys	Glu	Pro	Glu	His	Ser	Lys	325	330	335	
Gly	Gly	Gly	Arg	Val	Asp	Glu	Gly	Pro	Gln	Pro	Arg	Ser	Val	Glu	Pro	340	345	350	
Gln	Asp	Ala	Gly	Pro	Leu	Glu	Arg	Ser	Gln	Gly	Asp	Glu	Ala	Gly	Gly	355	360	365	
His	Gly	Glu	Asp	Arg	Pro	Glu	Pro	Leu	Ser	Pro	Lys	Glu	Ser	Lys	Lys	370	375	380	
Arg	Lys	Leu	Glu	Leu	Ser	Arg	Arg	Glu	Gln	Pro	Pro	Thr	Gly	Pro	Gly	385	390	395	400
Pro	Gln	Ser	Ala	Ser	Glu	Val	Glu	Lys	Ile	Ala	Leu	Asn	Leu	Glu	Gly	405	410	415	
Cys	Ala	Leu	Ser	Gln	Gly	Ser	Leu	Arg	Thr	Gly	Thr	Gln	Glu	Val	Gly	420	425	430	
Gly	Gln	Asp	Pro	Gly	Glu	Ala	Val	Gln	Pro	Cys	Arg	Gln	Pro	Leu	Gly	435	440	445	
Ala	Arg	Val	Ala	Asp	Lys	Val	Arg	Lys	Arg	Arg	Lys	Val	Asp	Glu	Gly	450	455	460	
Thr	Gly	Asp	Ser	Ala	Ala	Val	Ala	Ser	Gly	Gly	Ala	Gln	Thr	Leu	Ala	465	470	475	480
Leu	Ala	Gly	Ser	Pro	Ala	Pro	Ser	Gly	His	Pro	Lys	Ala	Gly	His	Ser	485	490	495	
Glu	Asn	Gly	Val	Glu	Glu	Asp	Thr	Glu	Gly	Arg	Thr	Gly	Pro	Lys	Glu	500	505	510	
Gly	Thr	Pro	Gly	Ser	Pro	Ser	Glu	Thr	Pro	Gly	Pro	Ser	Pro	Ala	Gly	515	520	525	
Pro	Ala	Gly	Asp	Glu	Pro	Ala	Lys	Thr	Pro	Ser	Glu	Thr	Pro	Gly	Pro	530	535	540	
Ser	Pro	Ala	Gly	Pro	Thr	Arg	Asp	Glu	Pro	Ala	Glu	Ser	Pro	Ser	Glu	545	550	555	560
Thr	Pro	Gly	Pro	Arg	Pro	Ala	Gly	Pro	Ala	Gly	Asp	Glu	Pro	Ala	Glu	565	570	575	
Ser	Pro	Ser	Glu	Thr	Pro	Gly	Pro	Arg	Pro	Ala	Gly	Pro	Ala	Gly	Asp	580	585	590	
Glu	Pro	Ala	Lys	Ile	Pro	Ser	Glu	Thr	Pro	Gly	Pro	Ser	Pro	Ala	Gly	595	600	605	
Pro	Thr	Arg	Asp	Glu	Pro	Ala	Glu	Ser	Pro	Ser	Glu	Thr	Pro	Gly	Pro	610	615	620	

a!
cont.

Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu
625 630 635 640

Thr Pro Gly Pro Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu
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Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr Arg Asp
660 665 670

Glu Pro Ala Lys Ala Gly Glu Ala Ala Glu Leu Gln Asp Ala Glu Val
675 680 685

Glu Ser Ser Ala Lys Ser Gly Lys Pro
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<211> 1601

<212> DNA

<213> Homo sapiens

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cont

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 <211> 461
 <212> PRT
 <213> Homo sapiens

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 Arg Ala Ala Arg Pro Ser Ser Phe Gln Ser Arg Met Leu Thr Gly Ser
 50 55 60
 Arg Asn Trp Arg Ala Thr Arg Asp Met Cys Arg Tyr Arg His Asn Tyr
 65 70 75 80
 Pro Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr Pro Asn Leu Ser
 85 90 95
 Phe Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu
 100 105 110
 Asp Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn
 115 120 125
 His Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn
 130 135 140

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Trp	His	Ala	Lys	Pro	Leu	Thr	Leu	Arg	Glu	Val	Glu	Val	Phe	Lys	Ser	145	150	155	160
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Gly	Phe	Tyr	Gly	Ile	Arg	Leu	Glu	Asp	Arg	Gly	Thr	Gly	Thr	Val	Gly	180	185	190	
Arg	Ala	Gln	Asn	Tyr	Gln	Lys	Arg	Phe	Gln	Asn	Leu	Asn	Trp	Arg	Ser	195	200	205	
His	Asn	Asn	Leu	Arg	Ile	Thr	Arg	Ile	Leu	Lys	Ser	Pro	Cys	Glu	Leu	210	215	220	
Ser	Leu	Glu	His	Phe	Gln	Ala	Pro	Leu	Val	Arg	Phe	Phe	Leu	Glu	Glu	225	230	235	240
Thr	Leu	Val	Arg	Arg	Glu	Leu	Pro	Gly	Val	Arg	Gln	Ser	Ala	Leu	Asp	245	250	255	
Tyr	Phe	Met	Phe	Ala	Val	Arg	Cys	Arg	His	Gln	Arg	Arg	Gln	Leu	Val	260	265	270	
His	Phe	Ala	Trp	Glu	His	Phe	Arg	Pro	Arg	Cys	Lys	Phe	Val	Trp	Gly	275	280	285	
Pro	Gln	Asp	Lys	Leu	Arg	Arg	Phe	Lys	Pro	Ser	Ser	Leu	Pro	His	Pro	290	295	300	
Leu	Glu	Gly	Ser	Arg	Lys	Val	Glu	Glu	Glu	Gly	Ser	Pro	Gly	Asp	Pro	305	310	315	320
Asp	His	Glu	Ala	Ser	Thr	Gln	Gly	Arg	Thr	Cys	Gly	Pro	Glu	His	Ser	325	330	335	
Lys	Gly	Gly	Gly	Arg	Val	Asp	Glu	Gly	Pro	Gln	Pro	Arg	Ser	Val	Glu	340	345	350	
Pro	Gln	Asp	Ala	Gly	Pro	Leu	Glu	Arg	Ser	Gln	Gly	Asp	Glu	Ala	Gly	355	360	365	
Gly	His	Gly	Glu	Asp	Arg	Pro	Glu	Pro	Leu	Ser	Pro	Lys	Glu	Ser	Lys	370	375	380	
Lys	Arg	Lys	Leu	Glu	Leu	Ser	Arg	Arg	Glu	Gln	Pro	Pro	Thr	Glu	Pro	385	390	395	400
Gly	Pro	Gln	Ser	Ala	Ser	Glu	Val	Glu	Lys	Ile	Ala	Leu	Asn	Leu	Glu	405	410	415	
Gly	Cys	Ala	Leu	Ser	Gln	Gly	Ser	Leu	Arg	Thr	Gly	Thr	Gln	Glu	Val	420	425	430	
Gly	Gly	Gln	Asp	Pro	Gly	Glu	Ala	Ser	Cys	Pro	Cys	Cys	Arg	Gly	Trp	435	440	445	

Al
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 <211> 2348
 <212> DNA
 <213> Homo sapiens

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1
 a
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 ccagaagccg cgaggccctc aggaagccc aaggcctgca gaagcctcct ggctggctg 2280
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 <211> 677
 <212> PRT
 <213> Homo sapiens

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 Ala Glu Asp Ala Glu Asp Glu Asp Cys Glu Asp Gly Glu Ala Ala Gly
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 Ala Arg Asp Ala Asp Ala Gly Asp Glu Asp Glu Glu Ser Glu Glu Pro
 35 40 45
 Arg Ala Ala Arg Pro Ser Ser Phe Gln Ser Arg Met Thr Gly Ser Arg
 50 55 60
 Asn Trp Arg Ala Thr Arg Asp Met Cys Arg Tyr Arg His Asn Tyr Pro
 65 70 75 80

Asp	Leu	Val	Glu	Arg 85	Asp	Cys	Asn	Gly	Asp 90	Thr	Pro	Asn	Leu	Ser 95	Phe
Tyr	Arg	Asn	Glu 100	Ile	Arg	Phe	Leu	Pro 105	Asn	Gly	Cys	Phe	Ile 110	Glu	Asp
Ile	Leu	Gln 115	Asn	Trp	Thr	Asp	Asn 120	Tyr	Asp	Leu	Leu	Glu 125	Asp	Asn	His
Ser	Tyr 130	Ile	Gln	Trp	Leu	Phe 135	Pro	Leu	Arg	Glu	Pro 140	Gly	Val	Asn	Trp
His 145	Ala	Lys	Pro	Leu	Thr 150	Leu	Arg	Glu	Val	Glu 155	Val	Phe	Lys	Ser	Ser 160
Gln	Glu	Ile	Gln	Glu 165	Arg	Leu	Val	Arg	Ala 170	Tyr	Glu	Leu	Met	Leu 175	Gly
Phe	Tyr	Gly	Ile 180	Arg	Leu	Glu	Asp	Arg 185	Gly	Thr	Gly	Thr	Val 190	Gly	Arg
Ala	Gln	Asn 195	Tyr	Gln	Lys	Arg	Phe 200	Gln	Asn	Leu	Asn	Trp 205	Arg	Ser	His
Asn	Asn 210	Leu	Arg	Ile	Thr	Arg 215	Ile	Leu	Lys	Ser	Pro 220	Cys	Glu	Leu	Ser
Leu 225	Glu	His	Phe	Gln	Ala 230	Pro	Leu	Val	Arg	Phe 235	Phe	Leu	Glu	Glu	Thr 240
Leu	Val	Arg	Arg	Glu 245	Leu	Pro	Gly	Val	Arg 250	Gln	Ser	Ala	Leu	Asp 255	Tyr
Phe	Met	Phe	Ala 260	Val	Arg	Cys	Arg	His 265	Gln	Arg	Arg	Gln	Leu 270	Val	His
Phe	Ala	Trp 275	Glu	His	Phe	Arg	Pro 280	Arg	Cys	Lys	Phe	Val 285	Trp	Gly	Pro
Gln	Asp 290	Lys	Leu	Arg	Arg	Phe 295	Lys	Pro	Ser	Ser	Leu 300	Pro	His	Pro	Leu
Glu 305	Gly	Ser	Arg	Lys	Val 310	Glu	Glu	Glu	Gly	Ser 315	Pro	Gly	Asp	Pro	Asp 320
His	Glu	Ala	Ser	Thr 325	Gln	Gly	Arg	Thr	Cys 330	Gly	Pro	Glu	His	Ser 335	Lys
Gly	Gly	Gly	Arg 340	Val	Asp	Glu	Gly	Pro 345	Gln	Pro	Arg	Ser	Val 350	Glu	Pro
Gln	Asp	Ala 355	Gly	Pro	Leu	Glu	Arg 360	Ser	Gln	Gly	Asp	Glu 365	Ala	Gly	Gly
His	Gly 370	Glu	Asp	Arg	Pro	Glu 375	Pro	Leu	Ser	Pro	Lys 380	Glu	Ser	Lys	Lys

Arg Lys Leu Glu Leu Ser Arg Arg Glu Gln Pro Pro Thr Glu Pro Gly
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 Pro Gln Ser Ala Ser Glu Val Glu Lys Ile Ala Leu Asn Leu Glu Gly
 405 410 415
 Cys Ala Leu Ser Gln Gly Ser Leu Arg Thr Gly Thr Gln Glu Val Gly
 420 425 430
 Gly Gln Asp Pro Gly Glu Ala Val Gln Pro Cys Arg Gln Pro Leu Gly
 435 440 445
 Ala Arg Val Ala Asp Lys Val Arg Lys Arg Arg Lys Val Asp Glu Gly
 450 455 460
 Ala Gly Asp Ser Ala Ala Val Ala Ser Gly Gly Ala Gln Thr Leu Ala
 465 470 475 480
 Leu Ala Gly Ser Pro Ala Pro Ser Gly His Pro Lys Ala Gly His Ser
 485 490 495
 Glu Asn Gly Val Glu Glu Asp Thr Glu Gly Arg Thr Gly Pro Lys Glu
 500 505 510
 Gly Thr Pro Gly Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly
 515 520 525
 Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
 530 535 540
 Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu
 545 550 555 560
 Thr Pro Gly Leu Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu
 565 570 575
 Thr Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr Arg Asp
 580 585 590
 Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro Arg Pro Ala Gly
 595 600 605
 Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
 610 615 620
 Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu
 625 630 635 640
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<212> DNA
<213> Homo sapiens

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 Arg Ala Ala Arg Pro Ser Ser Phe Gln Ser Arg Met Thr Gly Ser Arg
 50 55 60
 Asn Trp Arg Ala Thr Arg Asp Met Cys Arg Tyr Arg His Asn Tyr Pro
 65 70 75 80
 Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr Pro Asn Leu Ser Phe
 85 90 95

Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu Asp
 100 105 110
 Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn His
 115 120 125
 Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn Trp
 130 135 140
 His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu Val Phe Lys Ser Ser
 145 150 155 160
 Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr Glu Leu Met Leu Gly
 165 170 175
 Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr Gly Thr Val Gly Arg
 180 185 190
 Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu Asn Trp Arg Ser His
 195 200 205
 Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser Pro Cys Glu Leu Ser
 210 215 220
 Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe Phe Leu Glu Glu Thr
 225 230 235 240
 Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln Ser Ala Leu Asp Tyr
 245 250 255
 Phe Met Phe Ala Val Arg Cys Arg His Gln Arg Arg Gln Leu Val His
 260 265 270
 Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys Phe Val Trp Gly Pro
 275 280 285
 Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser Leu Pro His Pro Leu
 290 295 300
 Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Ser Pro Gly Asp Pro Asp
 305 310 315 320
 His Glu Ala Ser Thr Gln Gly Arg Thr Cys Gly Pro Glu His Ser Lys
 325 330 335
 Gly Gly Gly Arg Val Asp Glu Gly Pro Gln Pro Arg Ser Val Glu Pro
 340 345 350
 Gln Asp Ala Gly Pro Leu Glu Arg Ser Gln Gly Asp Glu Ala Gly Gly
 355 360 365
 His Gly Glu Asp Arg Pro Glu Pro Leu Ser Pro Lys Glu Ser Lys Lys
 370 375 380
 Arg Lys Leu Glu Leu Ser Arg Arg Glu Gln Pro Pro Thr Glu Pro Gly
 385 390 395 400

Pro Gln Ser Ala Ser Glu Val Glu Lys Ile Ala Leu Asn Leu Glu Gly
 405 410 415
 Cys Ala Leu Ser Gln Gly Ser Leu Arg Thr Gly Thr Gln Glu Val Gly
 420 425 430
 Gly Gln Asp Pro Gly Glu Ala Val Gln Pro Cys Arg Gln Pro Leu Gly
 435 440 445
 Ala Arg Val Ala Asp Lys Val Arg Lys Arg Arg Lys Val Asp Glu Gly
 450 455 460
 Ala Gly Asp Ser Ala Ala Val Ala Ser Gly Gly Ala Gln Thr Leu Ala
 465 470 475 480
 Leu Ala Gly Ser Pro Ala Pro Ser Gly His Pro Lys Ala Gly His Ser
 485 490 495
 Glu Asn Gly Val Glu Glu Asp Thr Glu Gly Arg Thr Gly Pro Lys Glu
 500 505 510
 Gly Thr Pro Gly Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly
 515 520 525
 Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
 530 535 540
 Arg Pro Ala Gly Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu
 545 550 555 560
 Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr Arg Asp Glu Pro Ala Glu
 565 570 575
 Ser Pro Ser Glu Thr Pro Gly Pro Arg Pro Ala Gly Pro Ala Gly Asp
 580 585 590
 Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro Arg Pro Ala Gly
 595 600 605
 Pro Ala Gly Asp Glu Pro Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro
 610 615 620
 Ser Pro Ala Gly Pro Thr Arg Asp Glu Pro Ala Lys Ala Gly Glu Ala
 625 630 635 640
 Ala Glu Leu Gln Asp Ala Glu Val Glu Ser Ser Ala Lys Ser Gly Lys
 645 650 655

Pro

<210> 13
 <211> 1232
 <212> DNA
 <213> Homo sapiens

<400> 13
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ggccgccggc gcgagggacg cggacgcagg ggacgaggac gaggagtcgg aggagccgcg 180
ggcggcgcgg cccagctcgt tccagtccag aatgacaggg tccagaaact ggcgagccac 240
gagggacatg tgtaggtatc ggcacaacta tccgatctg gtggaacgag actgcaatgg 300
ggacacgcca aacctgagtt tctacagaaa tgagatccgc ttcttgccca acggctgttt 360
cattgaggac attcttcaga actggacgga caactatgac ctcttgagg acaatcactc 420
ctacatccag tggctgtttc ctctgcgaga accaggagtg aactggcatg ccaagcccct 480
cacgctcagg gaggtcgagg tgtttaaaag ctcccaggag atccaggagc ggcttggtccg 540
ggcctacgag ctcatgctgg gcttctacgg gatccggctg gaggaccgag gcacgggcac 600
ggtgggcccga gcacagaact accagaagcg cttcagaacc tgaactggcg cagccacaac 660
aacctccgca tcacacgcat cctcaagtcg ccgtgtgagc tgagcctcga gcacttccag 720
gcgccactgg tccgcttctt cctggaggag acgctggtgc ggcgggagct gccgggggtg 780
cggcagagtg ccctggacta cttcatgttc gccgtgcgct gccgacacca gcgccgccag 840
ctggtgcact tcgcctggga gcacttccgg ccccgctgca agttcgtctg ggggccccaa 900
gacaagctgc ggaggttcaa gccagctct ctgccgcac cgctcgaggg ctccaggaag 960
gtggaggagg aaggacctgc aggggacgag ccagccgaga gcccatcgga gacccagggc 1020
cccagcccgg caggacctac aagggatgag ccagccaagg cgggggaggc agaagcctgc 1080
tgctgggctg tgtcttccca cccagctctc ccctgcgcc ctgtctttgt taatcgacct 1140
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ttttctgaat aaattcattt gactttcgaa aa 1232

<210> 14
<211> 392
<212> PRT
<213> Homo sapiens

<400> 14
Met Asp Asp Pro Asp Cys Asp Ser Thr Trp Glu Glu Asp Glu Glu Asp
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Ala Glu Asp Ala Glu Asp Glu Asp Cys Glu Asp Gly Glu Ala Ala Gly
20 25 30

Ala Arg Asp Ala Asp Ala Gly Asp Glu Asp Glu Glu Ser Glu Glu Pro
35 40 45

Arg Ala Ala Arg Pro Ser Ser Phe Gln Ser Arg Met Thr Gly Ser Arg
50 55 60

Asn Trp Arg Ala Thr Arg Asp Met Cys Arg Tyr Arg His Asn Tyr Pro
65 70 75 80

Asp Leu Val Glu Arg Asp Cys Asn Gly Asp Thr Pro Asn Leu Ser Phe
85 90 95

Tyr Arg Asn Glu Ile Arg Phe Leu Pro Asn Gly Cys Phe Ile Glu Asp
100 105 110

Ile Leu Gln Asn Trp Thr Asp Asn Tyr Asp Leu Leu Glu Asp Asn His
115 120 125

Ser Tyr Ile Gln Trp Leu Phe Pro Leu Arg Glu Pro Gly Val Asn Trp
130 135 140

His Ala Lys Pro Leu Thr Leu Arg Glu Val Glu Val Phe Lys Ser Ser
145 150 155 160

Gln Glu Ile Gln Glu Arg Leu Val Arg Ala Tyr Glu Leu Met Leu Gly
165 170 175

Phe Tyr Gly Ile Arg Leu Glu Asp Arg Gly Thr Gly Thr Val Gly Arg
180 185 190

Ala Gln Asn Tyr Gln Lys Arg Phe Gln Asn Leu Asn Trp Arg Ser His
195 200 205

Asn Asn Leu Arg Ile Thr Arg Ile Leu Lys Ser Pro Cys Glu Leu Ser
210 215 220

Leu Glu His Phe Gln Ala Pro Leu Val Arg Phe Phe Leu Glu Glu Thr
225 230 235 240

Leu Val Arg Arg Glu Leu Pro Gly Val Arg Gln Ser Ala Leu Asp Tyr
245 250 255

Phe Met Phe Ala Val Arg Cys Arg His Gln Arg Arg Gln Leu Val His
260 265 270

Phe Ala Trp Glu His Phe Arg Pro Arg Cys Lys Phe Val Trp Gly Pro
275 280 285

Gln Asp Lys Leu Arg Arg Phe Lys Pro Ser Ser Leu Pro His Pro Leu
290 295 300

Glu Gly Ser Arg Lys Val Glu Glu Glu Gly Pro Ala Gly Asp Glu Pro
305 310 315 320

Ala Glu Ser Pro Ser Glu Thr Pro Gly Pro Ser Pro Ala Gly Pro Thr
325 330 335

Arg Asp Glu Pro Ala Lys Ala Gly Glu Ala Glu Ala Cys Cys Leu Ala
340 345 350

Val Ser Ser His Pro Ala Leu Pro Cys Ala Pro Val Phe Val Asn Arg
355 360 365

Pro Phe Trp Ser Gly Gly Arg Arg Ala Gly Leu Ala Phe Leu Ser Leu
370 375 380

Met Pro Ser Lys Ala Phe Ser Glu
385 390

<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:antisense
primer for rat OGFr

<400> 15
gactcaggga cttagcttca tcc 23

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:scrambled
primer

<400> 16
atagatacta cgccggctgt cct 23

<210> 17
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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primer for human OGFr

<400> 17
ggtcgtccat gctcggctag aat 23

<210> 18
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:scrambled
primer

<400> 18
gtgcagtgca atgctctccg tga

23